



## SEQUENCE LISTING

RECEIVED

SEP 11 2002

TECH CENTER 1600/2900

<110> Nakayama, Naoki  
Wen, Duanzhi  
Han, Chun-ya  
He, Ching  
Yu, Dongyin

<120> Chordin-like Molecules and Uses Thereof

<130> 99,569-A

<140>

<141>

<150> 60/169,494

<151> 1999-12-07

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 1864

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (148)..(1146)

<220>

<221> sig\_peptide

<222> (148)..(213)

<400> 1

ccacgcgtcc ggagcgcccc agggagctca gagcttggtc aagcgtggca gcaggaggag 60

gccagtcccc agcttttagtc caccgctcct ctcttggtgag cccctgaatt gcattttgca 120

gtagctcgaa ggagaaaaaa gtagaag atg gat ggc atg aaa tac atc att tcc 174

Met Asp Gly Met Lys Tyr Ile Ile Ser

1

5

tta ttt ttc atc ttt gtt ttc cta gaa gga agc aaa aca gaa caa gta 222

Leu Phe Phe Ile Phe Val Phe Leu Glu Gly Ser Lys Thr Glu Gln Val

10

15

20

25

aaa cac tca gac aca tat tgc gtg ttt caa gac aag aag tat aga gtg 270

Lys His Ser Asp Thr Tyr Cys Val Phe Gln Asp Lys Lys Tyr Arg Val

30

35

40

ggg gag aaa tgg cat ccc tac ctg gaa ccg tat gga ctg gtt tac tgt 318

Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys

45

50

55

gtg aac tgc atc tgc tct gag aat ggg aat gtg ctt tgc agc cga gtc 366

Val	Asn	Cys	Ile	Cys	Ser	Glu	Asn	Gly	Asn	Val	Leu	Cys	Ser	Arg	Val	
	60						65					70				
aga	tgt	cca	agt	ctt	cat	tgc	ctt	tca	ccc	gtg	cat	att	cct	cat	ctc	414
Arg	Cys	Pro	Ser	Leu	His	Cys	Leu	Ser	Pro	Val	His	Ile	Pro	His	Leu	
	75					80				85						
tgt	tgc	ccc	cgc	tgc	cca	gac	tcc	tta	cca	cca	gtg	aac	aat	aag	gtg	462
Cys	Cys	Pro	Arg	Cys	Pro	Asp	Ser	Leu	Pro	Pro	Val	Asn	Asn	Lys	Val	
	90				95				100						105	
acc	agc	aag	tca	tgc	gaa	tac	aat	gga	acc	act	tac	caa	cat	gga	gaa	510
Thr	Ser	Lys	Ser	Cys	Glu	Tyr	Asn	Gly	Thr	Thr	Tyr	Gln	His	Gly	Glu	
				110				115						120		
ctg	ttc	ata	gct	gaa	ggg	ctc	ttt	cag	aac	cgg	caa	ccc	aat	cag	tgc	558
Leu	Phe	Ile	Ala	Glu	Gly	Leu	Phe	Gln	Asn	Arg	Gln	Pro	Asn	Gln	Cys	
			125					130					135			
agt	cag	tgt	agc	tgc	tcg	gag	ggg	aat	gta	tac	tgt	ggg	ctc	aag	act	606
Ser	Gln	Cys	Ser	Cys	Ser	Glu	Gly	Asn	Val	Tyr	Cys	Gly	Leu	Lys	Thr	
		140					145					150				
tgc	ccc	aaa	ctg	acc	tgt	gca	ttc	cca	gtc	tct	gtt	cca	gat	tct	tgc	654
Cys	Pro	Lys	Leu	Thr	Cys	Ala	Phe	Pro	Val	Ser	Val	Pro	Asp	Ser	Cys	
	155					160					165					
tgc	cga	gta	tgc	aga	ggg	gat	gca	gaa	tta	tcg	tgg	gaa	cat	gcg	gat	702
Cys	Arg	Val	Cys	Arg	Gly	Asp	Ala	Glu	Leu	Ser	Trp	Glu	His	Ala	Asp	
	170				175					180					185	
ggg	gat	atc	ttc	cgg	caa	cct	gcc	aac	aga	gaa	gca	aga	cat	tct	tac	750
Gly	Asp	Ile	Phe	Arg	Gln	Pro	Ala	Asn	Arg	Glu	Ala	Arg	His	Ser	Tyr	
				190				195						200		
ctc	cgt	tcc	ccc	tac	gat	cct	cca	cca	aac	aga	caa	gct	gga	ggg	ctt	798
Leu	Arg	Ser	Pro	Tyr	Asp	Pro	Pro	Pro	Asn	Arg	Gln	Ala	Gly	Gly	Leu	
			205					210					215			
ccc	cgc	ttt	cct	ggg	agc	aga	agt	cac	cgg	gga	gct	gtt	ata	gat	tcc	846
Pro	Arg	Phe	Pro	Gly	Ser	Arg	Ser	His	Arg	Gly	Ala	Val	Ile	Asp	Ser	
		220					225					230				
cag	caa	gca	tcc	ggg	acc	atc	gtg	cag	att	gtc	atc	aat	aac	aag	cac	894
Gln	Gln	Ala	Ser	Gly	Thr	Ile	Val	Gln	Ile	Val	Ile	Asn	Asn	Lys	His	
		235				240					245					
aaa	cat	gga	caa	gtg	tgt	gtt	tcc	aat	gga	aag	acc	tac	tct	cat	gga	942
Lys	His	Gly	Gln	Val	Cys	Val	Ser	Asn	Gly	Lys	Thr	Tyr	Ser	His	Gly	
	250				255					260					265	
gag	tcc	tgg	cac	cca	aat	cta	cga	gca	ttt	ggc	att	gtg	gaa	tgt	gta	990
Glu	Ser	Trp	His	Pro	Asn	Leu	Arg	Ala	Phe	Gly	Ile	Val	Glu	Cys	Val	
				270					275					280		
cta	tgc	act	tgt	aat	gtc	acc	aag	caa	gaa	tgt	aag	aaa	atc	cac	tgc	1038
Leu	Cys	Thr	Cys	Asn	Val	Thr	Lys	Gln	Glu	Cys	Lys	Lys	Ile	His	Cys	

1  
a  
cont.

285	290	295	
ccc aat cga tac ccc tgc aag tat cct caa aaa ata gat gga aag tgc			1086
Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys			
300	305	310	
tgc aag gtg tgc cca ggt aaa aag gca aaa ggt gca ttg gct gga ggc			1134
Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu Ala Gly Gly			
315	320	325	
cct gcc ttt ggt tgaatgagat tcacacatag tcctattcag tcttctttgt			1186
Pro Ala Phe Gly			
330			
tcacaaaac tataaatgac ctgtcttata gttctaacga taatagttct agcaagaatg			1246
aacttcatcc ttctgtcttc tgagacactg atggttgctt tgaaggaatt aactactcag			1306
agtttctttt gtctacaatg tcaaacacat gccaggttgc ttatcttggt cttgcttttc			1366
taaattagag agtttacgtt atcactgttt tagaaaaagt cacacctttc atgggtttaa			1426
tcaccaactc acttcaagac ataatccagt actcttttca gatgagatat aaatgagtta			1486
cagtggagag aaattagatt ctgatccaaa tgcacaaat ccacaagtat cttaccccat			1546
gtgaacattt taaagtttat tactgtgttc cacattgcta ttttaatttg caatttcttt			1606
ttaaattttc tgagatattg tatctgtata tacttatggg gtacagtatg ttaattcaat			1666
acaaatatac aaggtataat tgtcaaatca gggtaattat cattctctct cctctgattt			1726
tatccctaga ctcttctagt cattttaaaa tttatcatca attgggtttt tgatatggta			1786
actccactgt gctaaagaaa ccattcattc taatggcatt ttaggatcta ctatctaacc			1846
tctatctccc cttctggt			1864

<210> 2  
 <211> 333  
 <212> PRT  
 <213> Mus musculus

<400> 2  
 Met Asp Gly Met Lys Tyr Ile Ile Ser Leu Phe Phe Ile Phe Val Phe  
 1 5 10 15  
 Leu Glu Gly Ser Lys Thr Glu Gln Val Lys His Ser Asp Thr Tyr Cys  
 20 25 30  
 Val Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Lys Trp His Pro Tyr  
 35 40 45  
 Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu  
 50 55 60

Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Ser Leu His Cys  
 65 70 75 80  
 Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Asp  
 85 90 95  
 Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr  
 100 105 110  
 Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Ile Ala Glu Gly Leu  
 115 120 125  
 Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu  
 130 135 140  
 Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala  
 145 150 155 160  
 Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp  
 165 170 175  
 Ala Glu Leu Ser Trp Glu His Ala Asp Gly Asp Ile Phe Arg Gln Pro  
 180 185 190  
 Ala Asn Arg Glu Ala Arg His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro  
 195 200 205  
 Pro Pro Asn Arg Gln Ala Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg  
 210 215 220  
 Ser His Arg Gly Ala Val Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile  
 225 230 235 240  
 Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val  
 245 250 255  
 Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu  
 260 265 270  
 Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr  
 275 280 285  
 Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys  
 290 295 300  
 Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys  
 305 310 315 320  
 Lys Ala Lys Gly Ala Leu Ala Gly Gly Pro Ala Phe Gly  
 325 330

<210> 3  
 <211> 311  
 <212> PRT  
 <213> Mus musculus

<400> 3

Glu Gln Val Lys His Ser Asp Thr Tyr Cys Val Phe Gln Asp Lys Lys  
1 5 10 15

Tyr Arg Val Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu  
20 25 30

Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys  
35 40 45

Ser Arg Val Arg Cys Pro Ser Leu His Cys Leu Ser Pro Val His Ile  
50 55 60

Pro His Leu Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn  
65 70 75 80

Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln  
85 90 95

His Gly Glu Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro  
100 105 110

Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly  
115 120 125

Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro  
130 135 140

Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Ala Glu Leu Ser Trp Glu  
145 150 155 160

His Ala Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg  
165 170 175

His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro Pro Pro Asn Arg Gln Ala  
180 185 190

Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg Ser His Arg Gly Ala Val  
195 200 205

Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn  
210 215 220

Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr  
225 230 235 240

Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val  
245 250 255

Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys  
260 265 270

Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp  
275 280 285

Gly Lys Cys Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu  
290 295 300

Ala Gly Gly Pro Ala Phe Gly  
305 310

<210> 4  
<211> 3827  
<212> DNA  
<213> Rattus norvegicus

<220>  
<221> CDS  
<222> (142)..(1287)

<220>  
<221> sig\_peptide  
<222> (142)..(207)

<400> 4  
ccacgcgtcc gagcgcccca gggagctcag agcgtgtgca agcgtggcag aaggaagagg 60  
ccagtgccca gctttagccc accagtcccta ggagtctctg agctgcattt tgcagtagct 120  
caaaggagaa gagagtggaa a atg gaa ggc ata aaa tat atc gcc tcc ttg 171  
Met Glu Gly Ile Lys Tyr Ile Ala Ser Leu  
1 5 10  
gtt ttc ttc ttt gtt ttc ctg gaa gca agc aaa aca gag cca gta aaa 219  
Val Phe Phe Phe Val Phe Leu Glu Ala Ser Lys Thr Glu Pro Val Lys  
15 20 25  
cac tca gag aca tat tgc atg ttt caa gac aag aag tat aga gtt ggt 267  
His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly  
30 35 40  
gag aaa tgg cat ccc tac ctg gaa cca tat gga ctg gtt tac tgt gtg 315  
Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val  
45 50 55  
aac tgc atc tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga 363  
Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg  
60 65 70  
tgt cca act ctt cat tgc ctt tca ccc gtg cat att cct cat ctg tgt 411  
Cys Pro Thr Leu His Cys Leu Ser Pro Val His Ile Pro His Leu Cys  
75 80 85 90  
tgc ccc cgt tgc cca gac tcc tta cca ccg atg aac aat aag gtg acc 459  
Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Met Asn Asn Lys Val Thr  
95 100 105  
agc aag tcc tgc gaa tac aat ggg acc acc tac caa cac gga gag ctc 507  
Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu  
110 115 120  
ttc ata gct gaa ggg ctc ttt cag aac cgg cag ccc aat cag tgc agt 555  
Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser

125	130	135	
cag tgc agc tgc tgc gag ggg aat gtg tat tgt ggt ctc aag act tgc Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys 140 145 150			603
ccc aaa ctg acc tgt gca ttc cca gtc tct gtt cca gat tcc tgc tgc Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys 155 160 165 170			651
cga gta tgc aga ggg gat gga gaa tta tca tgg gaa cat tct gat gct Arg Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Ala 175 180 185			699
gat atc ttc cgg caa cct gcc aac aga gaa gca aga cat tct tac ctc Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr Leu 190 195 200			747
cgt tcc ccc tac gat cct cca cca agc aga caa gct gga ggt ctt cct Arg Ser Pro Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Pro 205 210 215			795
cgc ttt gct ggg agc aga agt cac cgg gga gct gtc att gat tct cag Arg Phe Ala Gly Ser Arg Ser His Arg Gly Ala Val Ile Asp Ser Gln 220 225 230			843
caa gca tca ggg acc atc gtg cag atc gtc atc aat aac aag cac aaa Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys 235 240 245 250			891
cat gga caa gtg tgt gtt tcc aat gga aag acc tat tct cac gga gaa His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu 255 260 265			939
tcc tgg cat tca aat cta cga gct ttt ggc att gtg gaa tgt gtt cta Ser Trp His Ser Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu 270 275 280			987
tgc act tgt aat gtc acc aag caa gaa tgt aag aaa atc cac tgc ccc Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro 285 290 295			1035
aat cga tac ccc tgc aag tat cct caa aaa tta gat gga aag tgc tgc Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Leu Asp Gly Lys Cys Cys 300 305 310			1083
aag gtg tgc cca gaa gaa cct cca agt caa aac ttt gac agc aaa ggt Lys Val Cys Pro Glu Glu Pro Pro Ser Gln Asn Phe Asp Ser Lys Gly 315 320 325 330			1131
tcc ttt tgt gga gaa gaa acc atg cct gta tat gag gct gtg ctc gtg Ser Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu Ala Val Leu Val 335 340 345			1179
gag gat gga gag aca gcc aga aaa gta gca ctg gag acc gag aaa cca Glu Asp Gly Glu Thr Ala Arg Lys Val Ala Leu Glu Thr Glu Lys Pro 350 355 360			1227

cct caa gta gta ggt tca cgt ttg gac tat tcg aaa ggg cat tct cca 1275  
 Pro Gln Val Val Gly Ser Arg Leu Asp Tyr Ser Lys Gly His Ser Pro  
 365 370 375

gca ctt cca cat tgagaagatt tccaaggaga tgtttgggga gctccatcat 1327  
 Ala Leu Pro His  
 380

ttcaagctgg tgactcgaac caccatgaac cagtggaaga tcttcgctga aggagaagct 1387  
 cagctcagcc agatgtgctc aagtcgggtg tgcagaacag aactggaaga tttgggtccag 1447  
 gttttgtacc tggagagacc tgaaaaggac cactgttaga caaaacagtc aggattgaat 1507  
 agtatcaatc aaggaaaccc aagctgcagc tggactgccg gcttacttta cttaagtcaa 1567  
 cagtgtcca aaaccccaaa gtcaacctca gtcaaattat ccagtcacag cacaccttgt 1627  
 tcctctatgt gcagcgggtg gccagccctc aaacatctcc tgtaaagaga atagaggagt 1687  
 cttaaatggt ttctgggggt ggggggagaa gggataggac tttgtggtac agctctat 1747  
 tctctgagaa tcacatttat ttgcaggtta aagtagaaaa gaaaaccact ttttagggat 1807  
 tctatgtaga aagtcacaag agagagagag agagaaattg ctgagtttga gttggatcat 1867  
 gccaaacaaa tttgtgtgaa atactttttg aatgttcaag tgtcttcctt actttaaaaa 1927  
 tgttattcag ttggtggttg aacagtcagg tgattatgga gcacatacct ataatatgtg 1987  
 gagacctggg ttctagtctc agaactgaca aaaaaatttc tctcctcata tctcacatgc 2047  
 acacacacac acacacacac acacacacac acacacacac acacacacac acagcacacg 2107  
 aaactgcatt tctttctggc tcctaaacac ctttgtggtt gttcgtatcc agggaaacaa 2167  
 actaaaaatg tatgcaaaaa actctgcctt caagcctttg aggcaggttg taagaaatca 2227  
 gccatagtct tagagtgaag aatgccattt gtgggtcttg tttccttcga agtactaaat 2287  
 acattttgcc tagtaatatc acttctcttt tcttatctgg caccctcatt aggaaggtag 2347  
 aatttggaaga actcatcaga aactaaattt attccaaaca aaatgacaat agaagaatat 2407  
 aactgataaa aaataaaata gtccattttt tgttttggtt ttacagctat aaatctaact 2467  
 gattaatagg ctaatgatgc tcactaattt tcttgaggca atagtcacct aggcagacac 2527  
 tttaggttga cacttttatt ctaaaagcct ttttaagggt aatttcctac tttgattaca 2587  
 ggagttgaaa tgtaactttt caaaaaggct caatccttac aagcttctca acatcagttc 2647  
 ttctgttaag tgctactgtt cattcacaga gctgagaatt ctggcaaaga tctttgtccc 2707  
 aaccttctt aatatecttg ccttattctt gagcatgggt tgcagcaggg attgtgacag 2767



cactacttct aaaatgttca ttgagagccc agtgcctcaa catcaatttt ccttcctgag 2827  
 gcttggtttt agaaatcacc ttttgaaaaa actataacta ttccctagca aagatcatag 2887  
 gttcactgga tctgtccatc tgccgagcat gaatgaactc acatgagtac taagaaatgt 2947  
 gaagatcaag aaattctata tttccctactc taagtggaaa aacatgatag gaaaaagtat 3007  
 gaagagtctg gtctttacta gaacctgaca gagaaggga ggctttgggg ccagggttc 3067  
 atgagacaaa cttcctgcca gccattaca cattctccca agaagagaag catagggcgt 3127  
 cctgggtctg aaagacactg aacattattg aagatgtgat ggggcaatgc caaccctctg 3187  
 ctgcttcctt cttggaggaa acactatttc cagagtgcgg agatcaatca caggctcctga 3247  
 aggaaagtgg tgattcctgt gctagacgat tcacccgcag ggaagggtgt gattccctgt 3307  
 ctagatgatt cactcacaaa cttcccgcc cagggtgttct ctgaaagctt agcctcaagg 3367  
 gaacaccta agagctcccc tacctacata aacctctgc tccaagtgt ggaactcacc 3427  
 tttctaaagc gctgtgggaa gcaggaactg ggcattctgt ctaagtcaat gtagaatttc 3487  
 tccagcgttt taatgctggg tagaatatag agcatagggg aaagggggcca aactgcctat 3547  
 agttagtaga gaaaaatgaa tgtggttctt ttgtgcattt atgtgtatca taaacacttg 3607  
 ggaaagcaaa aaccataagc accattttgc aactttatcc attttccagt tagctcatgt 3667  
 aaacgagcac gaataacaaa acagtattac tctttcgac ttctcacagg acatgtaccc 3727  
 aaatacggtc cttatttatg tagtcactgt gtttcaggac ttttacgtta ataaaatttt 3787  
 tatttaaaat tttaaaaaaa aaaaaaaaaa aaaaaaaaaa 3827

<210> 5  
 <211> 382  
 <212> PRT  
 <213> Rattus norvegicus

<400> 5  
 Met Glu Gly Ile Lys Tyr Ile Ala Ser Leu Val Phe Phe Phe Val Phe  
 1 5 10 15  
 Leu Glu Ala Ser Lys Thr Glu Pro Val Lys His Ser Glu Thr Tyr Cys  
 20 25 30  
 Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Lys Trp His Pro Tyr  
 35 40 45  
 Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu  
 50 55 60  
 Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Thr Leu His Cys  
 65 70 75 80

Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Asp  
 85 90 95  
 Ser Leu Pro Pro Met Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr  
 100 105 110  
 Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Ile Ala Glu Gly Leu  
 115 120 125  
 Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu  
 130 135 140  
 Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala  
 145 150 155 160  
 Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp  
 165 170 175  
 Gly Glu Leu Ser Trp Glu His Ser Asp Ala Asp Ile Phe Arg Gln Pro  
 180 185 190  
 Ala Asn Arg Glu Ala Arg His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro  
 195 200 205  
 Pro Pro Ser Arg Gln Ala Gly Gly Leu Pro Arg Phe Ala Gly Ser Arg  
 210 215 220  
 Ser His Arg Gly Ala Val Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile  
 225 230 235 240  
 Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val  
 245 250 255  
 Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Ser Asn Leu  
 260 265 270  
 Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr  
 275 280 285  
 Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys  
 290 295 300  
 Tyr Pro Gln Lys Leu Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu  
 305 310 315 320  
 Pro Pro Ser Gln Asn Phe Asp Ser Lys Gly Ser Phe Cys Gly Glu Glu  
 325 330 335  
 Thr Met Pro Val Tyr Glu Ala Val Leu Val Glu Asp Gly Glu Thr Ala  
 340 345 350  
 Arg Lys Val Ala Leu Glu Thr Glu Lys Pro Pro Gln Val Val Gly Ser  
 355 360 365  
 Arg Leu Asp Tyr Ser Lys Gly His Ser Pro Ala Leu Pro His  
 370 375 380

<210> 6  
 <211> 360  
 <212> PRT  
 <213> Rattus norvegicus

<400> 6  
 Glu Pro Val Lys His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys  
 1 5 10 15  
 Tyr Arg Val Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu  
 20 25 30  
 Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys  
 35 40 45  
 Ser Arg Val Arg Cys Pro Thr Leu His Cys Leu Ser Pro Val His Ile  
 50 55 60  
 Pro His Leu Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Met Asn  
 65 70 75 80  
 Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln  
 85 90 95  
 His Gly Glu Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro  
 100 105 110  
 Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly  
 115 120 125  
 Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro  
 130 135 140  
 Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu  
 145 150 155 160  
 His Ser Asp Ala Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg  
 165 170 175  
 His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro Pro Pro Ser Arg Gln Ala  
 180 185 190  
 Gly Gly Leu Pro Arg Phe Ala Gly Ser Arg Ser His Arg Gly Ala Val  
 195 200 205  
 Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn  
 210 215 220  
 Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr  
 225 230 235 240  
 Ser His Gly Glu Ser Trp His Ser Asn Leu Arg Ala Phe Gly Ile Val  
 245 250 255  
 Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys

a!  
 cont.

260 265 270

Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Leu Asp  
275 280 285

Gly Lys Cys Cys Lys Val Cys Pro Glu Glu Pro Pro Ser Gln Asn Phe  
290 295 300

Asp Ser Lys Gly Ser Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu  
305 310 315 320

Ala Val Leu Val Glu Asp Gly Glu Thr Ala Arg Lys Val Ala Leu Glu  
325 330 335

Thr Glu Lys Pro Pro Gln Val Val Gly Ser Arg Leu Asp Tyr Ser Lys  
340 345 350

Gly His Ser Pro Ala Leu Pro His  
355 360

<210> 7  
<211> 1496  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (132)..(1487)

<220>  
<221> sig\_peptide  
<222> (132)..(185)

<220>  
<221> sig\_peptide  
<222> (132)..(194)

<400> 7  
tagccagacc tcggacgaga gcgccccggg gagctcggag cgcgtgcacg cgtggcagac 60  
ggagaaggcc agtgcccagc ttgaagggtc tgccaccttt tgcagtgggtc caaatgagaa 120  
aaaagtggaa a atg gga ggc atg aaa tac atc ttt tcg ttg ttg ttc ttt 170  
Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe  
1 5 10

ctt ttg cta gaa gga ggc aaa aca gag caa gta aaa cat tca gag aca 218  
Leu Leu Leu Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr  
15 20 25

tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg cat 266  
Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His  
30 35 40 45

cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc tgc 314  
Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys

50										55					60					
tca	gag	aat	ggg	aat	gtg	ctt	tgc	agc	cga	gtc	aga	tgt	cca	aat	gtt	362				
Ser	Glu	Asn	Gly	Asn	Val	Leu	Cys	Ser	Arg	Val	Arg	Cys	Pro	Asn	Val					
			65			70						75								
cat	tgc	ctt	tct	cct	gtg	cat	att	cct	cat	ctg	tgc	tgc	cct	cgc	tgc	410				
His	Cys	Leu	Ser	Pro	Val	His	Ile	Pro	His	Leu	Cys	Cys	Pro	Arg	Cys					
			80			85						90								
cca	gaa	gac	tcc	tta	ccc	cca	gtg	aac	aat	aag	gtg	acc	agc	aag	tct	458				
Pro	Glu	Asp	Ser	Leu	Pro	Pro	Val	Asn	Asn	Lys	Val	Thr	Ser	Lys	Ser					
			95			100						105								
tgc	gag	tac	aat	ggg	aca	act	tac	caa	cat	gga	gag	ctg	ttc	gta	gct	506				
Cys	Glu	Tyr	Asn	Gly	Thr	Thr	Tyr	Gln	His	Gly	Glu	Leu	Phe	Val	Ala					
110						115						120			125					
gaa	ggg	ctc	ttt	cag	aat	cgg	caa	ccc	aat	caa	tgc	acc	cag	tgc	agc	554				
Glu	Gly	Leu	Phe	Gln	Asn	Arg	Gln	Pro	Asn	Gln	Cys	Thr	Gln	Cys	Ser					
			130						135						140					
tgt	tcg	gag	gga	aac	gtg	tat	tgt	ggg	ctc	aag	act	tgc	ccc	aaa	tta	602				
Cys	Ser	Glu	Gly	Asn	Val	Tyr	Cys	Gly	Leu	Lys	Thr	Cys	Pro	Lys	Leu					
			145						150						155					
acc	tgt	gcc	ttc	cca	gtc	tct	gtt	cca	gat	tcc	tgc	tgc	cgg	gta	tgc	650				
Thr	Cys	Ala	Phe	Pro	Val	Ser	Val	Pro	Asp	Ser	Cys	Cys	Arg	Val	Cys					
			160						165						170					
aga	gga	gat	gga	gaa	ctg	tca	tgg	gaa	cat	tct	gat	ggg	gat	atc	ttc	698				
Arg	Gly	Asp	Gly	Glu	Leu	Ser	Trp	Glu	His	Ser	Asp	Gly	Asp	Ile	Phe					
175						180						185								
cgg	caa	cct	gcc	aac	aga	gaa	gca	aga	cat	tct	tac	cac	cgc	tct	cac	746				
Arg	Gln	Pro	Ala	Asn	Arg	Glu	Ala	Arg	His	Ser	Tyr	His	Arg	Ser	His					
190						195						200			205					
tat	gat	cct	cca	cca	agc	cga	cag	gct	gga	ggg	ctg	tcc	cgc	ttt	cct	794				
Tyr	Asp	Pro	Pro	Pro	Ser	Arg	Gln	Ala	Gly	Gly	Leu	Ser	Arg	Phe	Pro					
			210						215						220					
ggg	gcc	aga	agt	cac	cgg	gga	gct	ctt	atg	gat	tcc	cag	caa	gca	tca	842				
Gly	Ala	Arg	Ser	His	Arg	Gly	Ala	Leu	Met	Asp	Ser	Gln	Gln	Ala	Ser					
			225						230						235					
gga	acc	att	gtg	caa	att	gtc	atc	aat	aac	aaa	cac	aag	cat	gga	caa	890				
Gly	Thr	Ile	Val	Gln	Ile	Val	Ile	Asn	Asn	Lys	His	Lys	His	Gly	Gln					
			240						245						250					
gtg	tgt	gtt	tcc	aat	gga	aag	acc	tat	tct	cat	ggc	gag	tcc	tgg	cac	938				
Val	Cys	Val	Ser	Asn	Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Ser	Trp	His					
255						260						265								
cca	aac	ctc	cgg	gca	ttt	ggc	att	gtg	gag	tgt	gtg	cta	tgt	act	tgt	986				
Pro	Asn	Leu	Arg	Ala	Phe	Gly	Ile	Val	Glu	Cys	Val	Leu	Cys	Thr	Cys					
270						275						280			285					

a!  
Cont

aat gtc acc aag caa gag tgt aag aaa atc cac tgc ccc aat cga tac 1034  
 Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr  
 290 295 300

ccc tgc aag tat cct caa aaa ata gac gga aag tgc tgc aag gtg tgt 1082  
 Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys  
 305 310 315

cca ggt aaa aaa gca aaa gaa gaa ctt cca ggc caa agc ttt gac aat 1130  
 Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe Asp Asn  
 320 325 330

aaa ggc tac ttc tgc ggg gaa gaa acg atg cct gtg tat gag tct gta 1178  
 Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu Ser Val  
 335 340 345

ttc atg gag gat ggg gag aca acc aga aaa ata gca ctg gag act gag 1226  
 Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu Thr Glu  
 350 355 360 365

aga cca cct cag gta gag gtc cac gtt tgg act att cga aag ggc att 1274  
 Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys Gly Ile  
 370 375 380

ctc cag cac ttc cat att gag aag atc tcc aag agg atg ttt gag gag 1322  
 Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe Glu Glu  
 385 390 395

ctt cct cac ttc aag ctg gtg acc aga aca acc ctg agc cag tgg aag 1370  
 Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln Trp Lys  
 400 405 410

atc ttc acc gaa gga gaa gct cag atc agc cag atg tgt tca agt cgt 1418  
 Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser Ser Arg  
 415 420 425

gta tgc aga aca gag ctt gaa gat tta gtc aag gtt ttg tac ctg gag 1466  
 Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr Leu Glu  
 430 435 440 445

aga tct gaa aag ggc cac tgt taggcaagg 1496  
 Arg Ser Glu Lys Gly His Cys  
 450

<210> 8  
 <211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 8  
 Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe Leu Leu Leu  
 1 5 10 15

Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met  
 20 25 30

Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu  
35 40 45  
Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn  
50 55 60  
Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His Cys Leu  
65 70 75 80  
Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp  
85 90 95  
Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr  
100 105 110  
Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu  
115 120 125  
Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu  
130 135 140  
Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala  
145 150 155 160  
Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp  
165 170 175  
Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro  
180 185 190  
Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr Asp Pro  
195 200 205  
Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg  
210 215 220  
Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile  
225 230 235 240  
Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val  
245 250 255  
Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu  
260 265 270  
Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr  
275 280 285  
Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys  
290 295 300  
Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys  
305 310 315 320  
Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr  
325 330 335

a!  
Cont.

Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu  
340 345 350

Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro  
355 360 365

Gln Val Glu Val His Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His  
370 375 380

Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His  
385 390 395 400

Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr  
405 410 415

Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser Ser Arg Val Cys Arg  
420 425 430

Thr Glu Leu Glu Asp Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu  
435 440 445

Lys Gly His Cys  
450

<210> 9

<211> 434

<212> PRT

<213> Homo sapiens

<400> 9

Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met Phe Gln  
1 5 10 15

Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu Glu Pro  
20 25 30

Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn  
35 40 45

Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His Cys Leu Ser Pro  
50 55 60

Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp Ser Leu  
65 70 75 80

Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly  
85 90 95

Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu Phe Gln  
100 105 110

Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu Gly Asn  
115 120 125

Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro

a  
cont.



130                      135                      140  
 Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Gly Glu  
 145                      150                      155                      160  
 Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn  
                     165                      170                      175  
 Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr Asp Pro Pro Pro  
                     180                      185                      190  
 Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg Ser His  
                     195                      200                      205  
 Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln  
                     210                      215                      220  
 Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn  
 225                      230                      235                      240  
 Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala  
                     245                      250                      255  
 Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln  
                     260                      265                      270  
 Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro  
                     275                      280                      285  
 Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys Lys Ala  
                     290                      295                      300  
 Lys Glu Glu Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys  
 305                      310                      315                      320  
 Gly Glu Glu Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly  
                     325                      330                      335  
 Glu Thr Thr Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val  
                     340                      345                      350  
 Glu Val His Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His Phe His  
                     355                      360                      365  
 Ile Glu Lys Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys  
                     370                      375                      380  
 Leu Val Thr Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly  
 385                      390                      395                      400  
 Glu Ala Gln Ile Ser Gln Met Cys Ser Ser Arg Val Cys Arg Thr Glu  
                     405                      410                      415  
 Leu Glu Asp Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly  
                     420                      425                      430  
 His Cys

<210> 10  
 <211> 431  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys  
 1 5 10 15  
 Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu  
 20 25 30  
 Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys  
 35 40 45  
 Ser Arg Val Arg Cys Pro Asn Val His Cys Leu Ser Pro Val His Ile  
 50 55 60  
 Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp Ser Leu Pro Pro Val  
 65 70 75 80  
 Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr  
 85 90 95  
 Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu Phe Gln Asn Arg Gln  
 100 105 110  
 Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys  
 115 120 125  
 Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val  
 130 135 140  
 Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Gly Glu Leu Ser Trp  
 145 150 155 160  
 Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala  
 165 170 175  
 Arg His Ser Tyr His Arg Ser His Tyr Asp Pro Pro Pro Ser Arg Gln  
 180 185 190  
 Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg Ser His Arg Gly Ala  
 195 200 205  
 Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile  
 210 215 220  
 Asn Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr  
 225 230 235 240  
 Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile  
 245 250 255

Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys  
 260 265 270  
 Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile  
 275 280 285  
 Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Glu Glu  
 290 295 300  
 Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu  
 305 310 315 320  
 Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr  
 325 330 335  
 Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val Glu Val His  
 340 345 350  
 Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His Phe His Ile Glu Lys  
 355 360 365  
 Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr  
 370 375 380  
 Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln  
 385 390 395 400  
 Ile Ser Gln Met Cys Ser Ser Arg Val Cys Arg Thr Glu Leu Glu Asp  
 405 410 415  
 Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly His Cys  
 420 425 430

<210> 11  
 <211> 1341  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(1341)

<220>  
 <221> sig\_peptide  
 <222> (1)..(54)

<220>  
 <221> sig\_peptide  
 <222> (1)..(63)

<400> 11  
 atg gga ggc atg aaa tac atc ttt tgc ttg ttg ttc ttt ctt ttg cta 48  
 Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe Leu Leu Leu  
 1 5 10 15

gaa gga ggc aaa aca gag caa gta aaa cat tca gag aca tat tgc atg 96

Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met	
20 25 30	
ttt caa gac aag aag tac aga gtg ggt gag aga tgg cat cct tac ctg	144
Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu	
35 40 45	
gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc tgc tca gag aat	192
Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn	
50 55 60	
ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat gtt cat tgc ctt	240
Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His Cys Leu	
65 70 75 80	
tct cct gtg cat att cct cat ctg tgc tgc cct cgc tgc cca gaa gac	288
Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp	
85 90 95	
tcc tta ccc cca gtg aac aat aag gtg acc agc aag tct tgc gag tac	336
Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr	
100 105 110	
aat ggg aca act tac caa cat gga gag ctg ttc gta gct gaa ggg ctc	384
Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu	
115 120 125	
ttt cag aat cgg caa ccc aat caa tgc acc cag tgc agc tgt tcg gag	432
Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu	
130 135 140	
gga aac gtg tat tgt ggt ctc aag act tgc ccc aaa tta acc tgt gcc	480
Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala	
145 150 155 160	
ttc cca gtc tct gtt cca gat tcc tgc tgc cgg gta tgc aga gga gat	528
Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp	
165 170 175	
gga gaa ctg tca tgg gaa cat tct gat ggt gat atc ttc cgg caa cct	576
Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro	
180 185 190	
gcc aac aga gaa gca aga cat tct tac cac cgc tct cac tat gat cct	624
Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr Asp Pro	
195 200 205	
cca cca agc cga cag gct gga ggt ctg tcc cgc ttt cct ggg gcc aga	672
Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg	
210 215 220	
agt cac cgg gga gct ctt atg gat tcc cag caa gca tca gga acc att	720
Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile	
225 230 235 240	
gtg caa att gtc atc aat aac aaa cac aag cat gga caa gtg tgt gtt	768
Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val	

245	250	255	
tcc aat gga aag acc tat tct cat ggc gag tcc tgg cac cca aac ctc			816
Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu			
260	265	270	
cgg gca ttt ggc att gtg gag tgt gtg cta tgt act tgt aat gtc acc			864
Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr			
275	280	285	
aag caa gag tgt aag aaa atc cac tgc ccc aat cga tac ccc tgc aag			912
Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys			
290	295	300	
tat cct caa aaa ata gac gga aag tgc tgc aag gtg tgt cca gaa gaa			960
Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu			
305	310	315	320
ctt cca ggc caa agc ttt gac aat aaa ggc tac ttc tgc ggg gaa gaa			1008
Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu			
325	330	335	
acg atg cct gtg tat gag tct gta ttc atg gag gat ggg gag aca acc			1056
Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr			
340	345	350	
aga aaa ata gca ctg gag act gag aga cca cct cag gta gag gtc cac			1104
Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val Glu Val His			
355	360	365	
gtt tgg act att cga aag ggc att ctc cag cac ttc cat att gag aag			1152
Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His Phe His Ile Glu Lys			
370	375	380	
atc tcc aag agg atg ttt gag gag ctt cct cac ttc aag ctg gtg acc			1200
Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr			
385	390	395	400
aga aca acc ctg agc cag tgg aag atc ttc acc gaa gga gaa gct cag			1248
Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln			
405	410	415	
atc agc cag atg tgt tca agt cgt gta tgc aga aca gag ctt gaa gat			1296
Ile Ser Gln Met Cys Ser Ser Arg Val Cys Arg Thr Glu Leu Glu Asp			
420	425	430	
tta gtc aag gtt ttg tac ctg gag aga tct gaa aag ggc cac tgt			1341
Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly His Cys			
435	440	445	

<210> 12  
 <211> 447  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe Leu Leu Leu  
 1 5 10 15  
 Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met  
 20 25 30  
 Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu  
 35 40 45  
 Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn  
 50 55 60  
 Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His Cys Leu  
 65 70 75 80  
 Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp  
 85 90 95  
 Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr  
 100 105 110  
 Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu  
 115 120 125  
 Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu  
 130 135 140  
 Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala  
 145 150 155 160  
 Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp  
 165 170 175  
 Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro  
 180 185 190  
 Ala Asn Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr Asp Pro  
 195 200 205  
 Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg  
 210 215 220  
 Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile  
 225 230 235 240  
 Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val  
 245 250 255  
 Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu  
 260 265 270  
 Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr  
 275 280 285  
 Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys  
 290 295 300

a!  
 cont

Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu  
305 310 315 320

Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu  
325 330 335

Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr  
340 345 350

Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val Glu Val His  
355 360 365

Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His Phe His Ile Glu Lys  
370 375 380

Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr  
385 390 395 400

Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln  
405 410 415

Ile Ser Gln Met Cys Ser Ser Arg Val Cys Arg Thr Glu Leu Glu Asp  
420 425 430

Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly His Cys  
435 440 445

<210> 13  
<211> 429  
<212> PRT  
<213> Homo sapiens

<400> 13  
Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met Phe Gln  
1 5 10 15

Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu Glu Pro  
20 25 30

Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn  
35 40 45

Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val His Cys Leu Ser Pro  
50 55 60

Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp Ser Leu  
65 70 75 80

Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly  
85 90 95

Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu Phe Gln  
100 105 110

Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu Gly Asn  
115 120 125

a!  
cont.

Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro  
 130 135 140  
 Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Gly Glu  
 145 150 155 160  
 Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn  
 165 170 175  
 Arg Glu Ala Arg His Ser Tyr His Arg Ser His Tyr Asp Pro Pro Pro  
 180 185 190  
 Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg Ser His  
 195 200 205  
 Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln  
 210 215 220  
 Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn  
 225 230 235 240  
 Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala  
 245 250 255  
 Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln  
 260 265 270  
 Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro  
 275 280 285  
 Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu Leu Pro  
 290 295 300  
 Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met  
 305 310 315 320  
 Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys  
 325 330 335  
 Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp  
 340 345 350  
 Thr Ile Arg Lys Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser  
 355 360 365  
 Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr  
 370 375 380  
 Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser  
 385 390 395 400  
 Gln Met Cys Ser Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val  
 405 410 415  
 Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly His Cys  
 420 425



<210> 14  
 <211> 426  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Glu Gln Val Lys His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys  
 1 5 10 15  
 Tyr Arg Val Gly Glu Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu  
 20 25 30  
 Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys  
 35 40 45  
 Ser Arg Val Arg Cys Pro Asn Val His Cys Leu Ser Pro Val His Ile  
 50 55 60  
 Pro His Leu Cys Cys Pro Arg Cys Pro Glu Asp Ser Leu Pro Pro Val  
 65 70 75 80  
 Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr  
 85 90 95  
 Gln His Gly Glu Leu Phe Val Ala Glu Gly Leu Phe Gln Asn Arg Gln  
 100 105 110  
 Pro Asn Gln Cys Thr Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys  
 115 120 125  
 Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val  
 130 135 140  
 Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Gly Glu Leu Ser Trp  
 145 150 155 160  
 Glu His Ser Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala  
 165 170 175  
 Arg His Ser Tyr His Arg Ser His Tyr Asp Pro Pro Pro Ser Arg Gln  
 180 185 190  
 Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg Ser His Arg Gly Ala  
 195 200 205  
 Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile  
 210 215 220  
 Asn Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr  
 225 230 235 240  
 Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile  
 245 250 255  
 Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys

260	265	270
Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile		
275	280	285
Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu Leu Pro Gly Gln Ser		
290	295	300
Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr		
305	310	315
Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu		
325	330	335
Glu Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg		
340	345	350
Lys Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met		
355	360	365
Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser		
370	375	380
Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys		
385	390	395
Ser Ser Arg Val Cys Arg Thr Glu Leu Glu Asp Leu Val Lys Val Leu		
405	410	415
Tyr Leu Glu Arg Ser Glu Lys Gly His Cys		
420	425	

<210> 15  
 <211> 948  
 <212> PRT  
 <213> Mus musculus

<400> 15  
 Met Pro Ser Leu Pro Ala Pro Pro Ala Pro Arg Leu Leu Leu Gly Leu  
 1 5 10 15  
 Leu Leu Leu Gly Ser Arg Pro Ala Ser Gly Thr Gly Pro Glu Pro Pro  
 20 25 30  
 Ala Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val Arg Gly Ala  
 35 40 45  
 Ala Gly Cys Ser Phe Gly Gly Lys Val Tyr Ala Leu Asp Glu Thr Trp  
 50 55 60  
 His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys  
 65 70 75 80  
 Ala Cys Glu Ala Pro Gln Trp Ala Arg Arg Gly Arg Gly Pro Gly Arg  
 85 90 95

Val Ser Cys Lys Asn Ile Lys Pro Gln Cys Pro Thr Leu Ala Cys Arg  
 100 105 110  
 Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu  
 115 120 125  
 Arg Ser Asn Leu Asp Pro Gln Pro Ala Gly Leu Val Phe Glu Tyr Pro  
 130 135 140  
 Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Val  
 145 150 155 160  
 Gly Glu Arg Thr Arg Ala Asp Gly His Thr Asp Phe Val Ala Leu Leu  
 165 170 175  
 Thr Gly Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu  
 180 185 190  
 Arg Ser Ser Leu Arg Phe Ser Val Ser Tyr Gln Arg Leu Asp Arg Pro  
 195 200 205  
 Ser Arg Val Arg Phe Thr Asp Pro Thr Gly Asn Ile Leu Phe Glu His  
 210 215 220  
 Pro Ala Thr Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala  
 225 230 235 240  
 Val Pro Arg Leu Ser Val Arg Leu Leu Arg Ala Glu Gln Leu Arg Val  
 245 250 255  
 Ala Leu Val Thr Ser Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu  
 260 265 270  
 Ile Trp Gln Gly Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr  
 275 280 285  
 Leu Glu Asp Pro Leu Gln Arg Gly Val Gly Gly Ile Ala Leu Leu Thr  
 290 295 300  
 Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe Arg Gly  
 305 310 315 320  
 Leu Leu Gly Gly Leu Ala Gln Ala Pro Leu Lys Leu Gln Ile Leu His  
 325 330 335  
 Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala Asn Thr Ser Ala Gln Glu  
 340 345 350  
 Pro Gly Phe Ala Glu Val Leu Pro Ser Leu Thr Asp Gln Glu Met Asp  
 355 360 365  
 Trp Leu Glu Leu Gly Glu Leu Gln Met Val Leu Glu Lys Ala Gly Gly  
 370 375 380  
 Pro Glu Leu Arg Ile Ser Gly Tyr Ile Thr Thr Arg Gln Ser Cys Asp  
 385 390 395 400

a'  
 Cont

Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro Val Gln  
 405 410 415  
 Thr Gly Ala Ala Gly Ser Ala Ser Phe Ile Leu Leu Gly Asn Gly Ser  
 420 425 430  
 Leu Ile Tyr Gln Val Gln Val Val Gly Thr Gly Ser Glu Val Val Ala  
 435 440 445  
 Met Thr Leu Glu Thr Lys Pro Gln Arg Lys Asn Gln Arg Thr Val Leu  
 450 455 460  
 Cys His Met Ala Gly Leu Gln Pro Gly Gly His Met Ala Val Gly Met  
 465 470 475 480  
 Cys Ser Gly Leu Gly Ala Arg Gly Ala His Met Leu Leu Gln Asn Glu  
 485 490 495  
 Leu Phe Leu Asn Val Gly Thr Lys Asp Phe Pro Asp Gly Glu Leu Arg  
 500 505 510  
 Gly His Val Thr Ala Leu Cys Tyr Ser Gly His Ser Ala Arg Tyr Asp  
 515 520 525  
 Arg Leu Pro Val Pro Leu Ala Gly Ala Leu Val Leu Pro Pro Val Arg  
 530 535 540  
 Ser Gln Ala Ala Gly His Ala Trp Leu Ser Leu Asp Thr His Cys His  
 545 550 555 560  
 Leu His Tyr Glu Val Leu Leu Ala Gly Leu Gly Gly Ser Glu Gln Gly  
 565 570 575  
 Thr Val Thr Ala His Leu Leu Gly Pro Pro Gly Met Pro Gly Pro Gln  
 580 585 590  
 Arg Leu Leu Lys Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys  
 595 600 605  
 Asp Leu Glu Pro Val Leu Leu Arg His Leu Ala Gln Gly Thr Ala Ser  
 610 615 620  
 Leu Leu Ile Thr Thr Lys Ser Ser Pro Arg Gly Glu Leu Arg Gly Gln  
 625 630 635 640  
 Val His Ile Ala Ser Gln Cys Glu Ala Gly Gly Leu Arg Leu Ala Ser  
 645 650 655  
 Glu Gly Val Gln Met Pro Leu Ala Pro Asn Gly Glu Ala Ala Thr Ser  
 660 665 670  
 Pro Met Leu Pro Ala Gly Pro Gly Pro Glu Ala Pro Val Pro Ala Lys  
 675 680 685  
 His Gly Ser Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys Phe Phe Glu  
 690 695 700

a!  
 cont.

Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro Asn Tyr Asp Pro  
705 710 715 720

Leu Cys Ser Leu Cys Ile Cys Gln Arg Arg Thr Val Ile Cys Asp Pro  
725 730 735

Val Val Cys Pro Pro Pro Ser Cys Pro His Pro Val Gln Ala Leu Asp  
740 745 750

Gln Cys Cys Pro Val Cys Pro Glu Lys Gln Arg Ser Arg Asp Leu Pro  
755 760 765

Ser Leu Pro Asn Leu Glu Pro Gly Glu Gly Cys Tyr Phe Asp Gly Asp  
770 775 780

Arg Ser Trp Arg Ala Ala Gly Thr Arg Trp His Pro Val Val Pro Pro  
785 790 795 800

Phe Gly Leu Ile Lys Cys Ala Val Cys Thr Cys Lys Gly Ala Thr Gly  
805 810 815

Glu Val His Cys Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln  
820 825 830

Pro Val Arg Ala Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly  
835 840 845

Ser Gly Thr Asn Ala Lys Leu Gly Asp Pro Met Gln Ala Asp Gly Pro  
850 855 860

Arg Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Asn Gln Ser Trp  
865 870 875 880

His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys Arg  
885 890 895

Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser Pro Pro  
900 905 910

Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys Cys Ser His Cys Thr  
915 920 925

Ala Gln Arg Ser Ser Glu Thr Arg Thr Leu Pro Glu Leu Glu Lys Glu  
930 935 940

Ala Glu His Ser  
945

<210> 16

<211> 176

<212> PRT

<213> Rattus norvegicus

<400> 16

Gly Gly Leu Arg Leu Ala Ser Glu Gly Val Arg Met Ser Leu Ala Pro  
1 5 10 15

Asn Gly Glu Ala Ala Thr Ser Pro Met Leu Pro Ala Gly Pro Gly Pro  
                   20                                  25                                  30  
 Glu Ala Pro Val Pro Ala Lys His Gly Ser Ser Gly Arg Pro Arg Asp  
                   35                                  40                                  45  
 Pro Asn Thr Cys Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg  
                   50                                  55                                  60  
 Trp Ala Pro Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg  
                   65                                  70                                  75                                  80  
 Arg Thr Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Arg Cys Ser  
                                   85                                  90                                  95  
 Gln Pro Val Gln Ala Leu Asp Gln Trp Cys Pro Val Cys Ser Glu Lys  
                                   100                                  105                                  110  
 Gln Arg Ser Arg Asp Leu Ser Ser Leu Pro Asn Leu Glu Pro Gly Glu  
                                   115                                  120                                  125  
 Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala Gly Thr Arg  
                   130                                  135                                  140  
 Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys Cys Gly Val Cys  
                   145                                  150                                  155                                  160  
 Thr Cys Lys Gly Val Asn Gly Glu Val His Ser Glu Lys Val Gln Cys  
                                   165                                  170                                  175

<210> 17  
 <211> 801  
 <212> PRT  
 <213> Homo sapiens

<400> 17  
 Gln Val Ala Ala Gly His Cys Cys Gln Thr Cys Pro Gln Glu Arg Ser  
                   1                                  5                                  10                                  15  
 Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu Tyr Pro Arg Asp  
                                   20                                  25                                  30  
 Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala Glu Glu  
                   35                                  40                                  45  
 Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu Thr Gly  
                   50                                  55                                  60  
 Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Ala Ser Leu Leu Arg Ser  
                   65                                  70                                  75                                  80  
 Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro Thr Arg  
                                   85                                  90                                  95  
 Ile Arg Phe Ser Asp Pro Asn Gly Ser Val Leu Phe Glu His Pro Ala

100	105	110
Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala Val Pro 115 120 125		
Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His Val Ala Leu 130 135 140		
Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu Ile Arg 145 150 155 160		
His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr Leu Glu 165 170 175		
Gly Pro Pro Gln Gln Gly Val Gly Gly Ile Thr Leu Leu Thr Leu Ser 180 185 190		
Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe Arg Gly Leu Leu 195 200 205		
Glu Pro Arg Ser Gly Gly Leu Thr Gln Val Pro Leu Arg Leu Gln Ile 210 215 220		
Leu His Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala Asn Val Ser Ala 225 230 235 240		
Gln Glu Pro Gly Phe Ala Glu Val Leu Pro Asn Leu Thr Val Gln Glu 245 250 255		
Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala Leu Glu Trp Ala 260 265 270		
Gly Arg Pro Gly Leu Arg Ile Ser Gly His Ile Ala Ala Arg Lys Ser 275 280 285		
Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu Ile Pro 290 295 300		
Val Gln Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu Gly Asn 305 310 315 320		
Gly Ser Leu Ile Tyr Gln Ala Val Gly Ile Cys Pro Gly Leu Gly Ala 325 330 335		
Arg Gly Ala His Met Leu Leu Gln Asn Glu Leu Phe Leu Asn Val Gly 340 345 350		
Thr Lys Asp Phe Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu 355 360 365		
Pro Tyr Cys Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu 370 375 380		
Ala Gly Ala Leu Val Leu Pro Pro Val Lys Ser Gln Ala Ala Gly His 385 390 395 400		
Ala Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu		

a!  
cont





705	710	715	720
Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp His Pro Ser Val Pro			
725		730	735
Pro Phe Gly Glu Met Ser Cys Ile Thr Cys Arg Cys Gly Ala Gly Val			
740	745		750
Pro His Cys Glu Arg Asp Asp Cys Ser Leu Pro Leu Ser Cys Gly Ser			
755	760		765
Gly Lys Glu Ser Arg Cys Cys Ser Arg Cys Thr Ala His Arg Arg Pro			
770	775	780	
Ala Pro Glu Thr Arg Thr Asp Pro Glu Leu Glu Lys Glu Ala Glu Gly			
785	790	795	800
Ser			

<210> 18  
 <211> 11  
 <212> PRT  
 <213> Human immunodeficiency virus type 1

<400> 18  
 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg  
 1 5 10

<210> 19  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Internalizing  
 domain derived from HIV tat protein

<400> 19  
 Gly Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg  
 1 5 10 15

<210> 20  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer  
 2125-05

<400> 20  
 agtgcaccagc tttagtccac

20

*a1*  
*cont.*

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2125-06

<400> 21  
gagatgagga atatgcacgg

20

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2127-58

<400> 22  
gacatctgac tcggctgc

18

<210> 23  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2212-48

<400> 23  
tcacgcagta aaccaac

17

*a1*  
*cont*  
<210> 24  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2235-53

<400> 24  
cggaattcgc caccatggga ggcataaat acatcttt

38

<210> 25  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer  
2235-54

<400> 25

cgcggatcca cagtggccct tttcagatct etc

33

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 26

ttaccaccag tgaacaataa gg

22

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 27

cttgagacca cagtatacat tc

22

<210> 28

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

agtgccccagc tttagtccac

20

<210> 29

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 29

gttctgtttt gcttccttct ag

22

<210> 30

a!  
cont.

<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2149-76

<400> 30  
gctagcggcc gcgccaccat ggatggcatg aaatacatca tttc

44

<210> 31  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2149-77

<400> 31  
ggtaccggat ccaccaaagg cagggcctcc agc

33

<210> 32  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2170-06

<400> 32  
gctagcggcc gcgccaccat gccgagcctc ccggccccg

39

<210> 33  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
2170-07

<400> 33  
ggatccgtcg acggagtgtc ccgcttcttt ctccag

36

<210> 34  
<211> 345  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Murine  
CHL-FLAG

<220>

<221> SIGNAL

<222> (1)..(22)

<220>

<221> SITE

<222> (334)..(345)

<223> FLAG domain

<400> 34

Met Asp Gly Met Lys Tyr Ile Ile Ser Leu Phe Phe Ile Phe Val Phe  
1 5 10 15

Leu Glu Gly Ser Lys Thr Glu Gln Val Lys His Ser Asp Thr Tyr Cys  
20 25 30

Val Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Lys Trp His Pro Tyr  
35 40 45

Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu  
50 55 60

Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Ser Leu His Cys  
65 70 75 80

Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Asp  
85 90 95

Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr  
100 105 110

Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Ile Ala Glu Gly Leu  
115 120 125

Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu  
130 135 140

Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala  
145 150 155 160

Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp  
165 170 175

Ala Glu Leu Ser Trp Glu His Ala Asp Gly Asp Ile Phe Arg Gln Pro  
180 185 190

Ala Asn Arg Glu Ala Arg His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro  
195 200 205

Pro Pro Asn Arg Gln Ala Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg  
210 215 220

Ser His Arg Gly Ala Val Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile  
225 230 235 240

a!  
cont.

Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val  
245 250 255

Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu  
260 265 270

Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr  
275 280 285

Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys  
290 295 300

Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys  
305 310 315 320

Lys Ala Lys Gly Ala Leu Ala Gly Gly Pro Ala Phe Gly Gly Ser Gly  
325 330 335

Thr Asp Tyr Lys Asp Asp Asp Asp Lys  
340 345

<210> 35  
<211> 323  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Murine  
CHL-FLAG

<220>  
<221> SITE  
<222> (312)..(323)  
<223> FLAG domain

<400> 35  
Glu Gln Val Lys His Ser Asp Thr Tyr Cys Val Phe Gln Asp Lys Lys  
1 5 10 15

Tyr Arg Val Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu  
20 25 30

Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys  
35 40 45

Ser Arg Val Arg Cys Pro Ser Leu His Cys Leu Ser Pro Val His Ile  
50 55 60

Pro His Leu Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn  
65 70 75 80

Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln  
85 90 95

His Gly Glu Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro

100                      105                      110  
 Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly  
           115                      120                      125  
 Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro  
           130                      135                      140  
 Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Ala Glu Leu Ser Trp Glu  
           145                      150                      155                      160  
 His Ala Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg  
                           165                      170                      175  
 His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro Pro Pro Asn Arg Gln Ala  
                           180                      185                      190  
 Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg Ser His Arg Gly Ala Val  
           195                      200                      205  
 Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn  
           210                      215                      220  
 Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr  
           225                      230                      235                      240  
 Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val  
                           245                      250                      255  
 Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys  
           260                      265                      270  
 Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp  
           275                      280                      285  
 Gly Lys Cys Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu  
           290                      295                      300  
 Ala Gly Gly Pro Ala Phe Gly Gly Ser Gly Thr Asp Tyr Lys Asp Asp  
           305                      310                      315                      320  
 Asp Asp Lys

<210> 36  
 <211> 962  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Murine  
           CHD-FLAG

<220>  
 <221> SIGNAL  
 <222> (1) .. (26)

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☐ FADED TEXT OR DRAWING
- ☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☒ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**